

FIG. 1

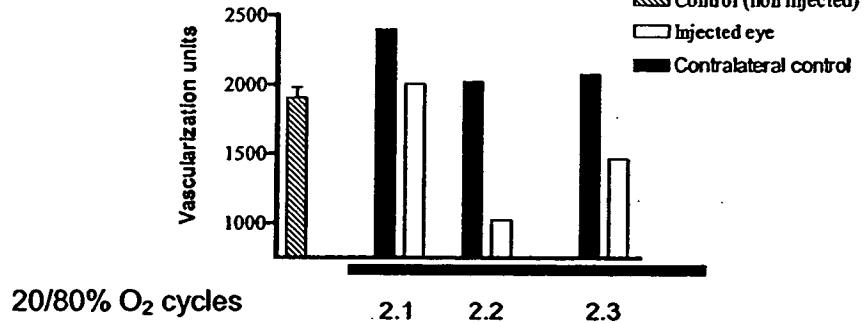
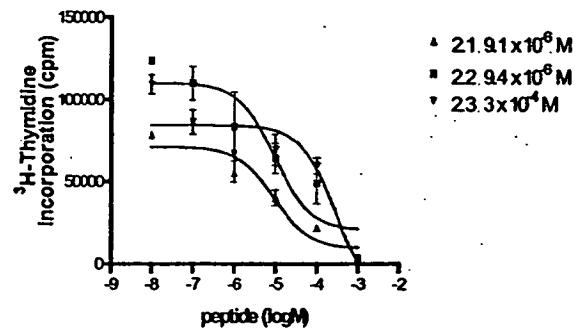
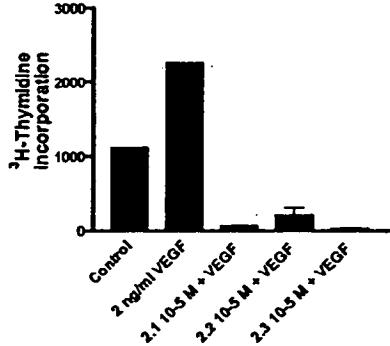


FIG. 2

MQSKVLLAVALWLCVETRAASVGLPSVSLDLPLRSIQKDILTIKANTTLQITCRGQRDID 60  
 ↑  
 Ig-like 1

WLWPNNQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVVQD 120

YRSPIIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWD 180  
 ↑  
 Ig-like 2

SKKGFTIPSYMISYAGMVFCEAKINDESYSQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE 240  
 ↑  
 Ig-like 3

KLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS 300

DQGLYTCAASSGLMTKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP 360  
 ↑  
 Ig-like 4

EIKWYKNGIPLSNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKERQSHVVSLLVVYVP 420

PQIGEKLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEEECANEPSQAVSVTNPY 480  
 ↑  
 Ig-like 5

PCEEWRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGE 540

RVISFHVTGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGEELPT 600  
 ↑  
 Ig-like 6

PVCKNLDTLWKLNATMFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKRHCVVRQLT 660

↓  
 Ig-like 7

VLERVAPITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR 720

Figure 3

NLTIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLEIILVGTAVIAMFFWL 780

LLVIIILRTVKRANGGELKTYGLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPL 840

GRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNVN 900

LLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVDLK 960

RRLDSITSSQSSASSGFVEEKSLSDVEEEAPEDLYKDFLTLEHLICYSFQVAKGMEFLA 1020

SRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGARLPLKWMAPETIFDR 1080

VYTIQSDVWSFGVLLWEIFSILGASPYPGVKIDEEPCRRLKEGTRMRAPDTTPEMYQTML 1140

DCWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVS 1200

CMEEEEVCDPKFHDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEPVKVIPDDNQTDS 1260

GMVLASEELKTLERTKLSPSPGGMVPSKSRESVASEGSNQTSGYQSGYHSDDTDTTVYS 1320

SEEAKLLKLIEIGVQTGSTAQILQPDSGTTLSSPPV

FIG. 3 continued

MKVLLRLICFIALLISSLEADCKKEREKKIILVSSANEIDVRPCPLNPNEHKGTITWYKD 60

↑  
Ig-like domain 1 →

DSKTPVSTEQASRIHQHKEKLWFVPAKVEDSGHYYCVRNSSYCLRIKISAKFVENEPNL 120

CYNAQAIPKQKLPVAGDGLVCPYMEFFKNENNELPKLQWYKDCKPLLDNIHPSGVKDR 180

↑  
Ig-like 2 →

LIVMNVAEKHRGNYTCHASYTYLGKQYPITRVICEITLEENKPTRPVIVSPANETMEVDL 240

↑  
Ig-like 3 →  
GSQIQOLICNVTGQLSDIAYKWNGSVIDEDDPVLGEDYYSVENPANKRRSTLITVLNISE 300

IERSFYKHPFTCFAKNTHG [DAAYIQLIYPVTNFQKHMIG] CVTLTVIIVCSVFIYKIFK 360

IDIVLWYRDSCYDFLPIKASDGKTYDAYILYPKTVGEGSTSACDIFVFVVLPEVLEKQCG 420

YKLFIFYGRDDYVGKDIVEVINENVKSRRLLLILVRETSGFSWLGGSSBQIAMYNALVQ 480

DGIKVVLLELEKIQDYKKMPESIKPIKQHGAIWSGDFTQGPQSAKTRFWKNVRYHMPV 540

QRRSPSSKHQOLLSPATKEKLQREAHVPLG 569

FIG. 4

MTLLWCVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHPLKFNYST 60

↑ Ig-like 1 domain →

AHSAGLTLIWWTRQDRDLESPINFRLPENRISKEKDVLWPRPTLLNDTGNYTCMLRNTT 120

YCSKVAFPLEVVQKDSCFNSPMQLPVHKLYIEYGIQRITCPNVGDGYPPSSVKPTITWYMG 180

↑ Ig-like 2 →

CYKIQNFNNVIPEGMNLSPFLIALISNNNGNYTCVVTYPENGRTFHLLRTLTVKVVGSPKNA 240

VPPVIHSPNDHVYYEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKRPDDITIDVTINE 300

↑ Ig-like 3 →

SISHSRTEDETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKVQKVPAPRTVEL 360  
Juxtamembranous

ACGFGATVLLVVILIVYYHVVWLEMVLFYRAHFGTDETILDGKEYDIYVSYARNAEEEF 420

VLLTLRGVLEN~~EFGY~~KLCIFDRDSLPGGIVTDETLSFIQKSRRLLVVLS~~PNV~~LQGTQAL 480

LELKAGLENMASRGNINVILVQYKAVKETKV~~KELKRAKT~~TVLTVIKWKGEKSKYPQGRFWK 540

QLQVAMPVKKSPRSSSDEQGLSYSSLKNV

FIG. 5

MKSGSCGGSPSLWGLLFLSAALSLWPTSGEICGPGIDIRNDYQQLKRLENCTVIEGYLH 60

Chaîne α →

ILLISKAEDYRSYRFPKLTIVITEYLLLFRVAGLESIGDLFPNLTVIRGWKLFYNYALVIF 120

EMTNLKDIGLYNLRNITRGAIRIEKKNADLCYLSTVDWSLILDAVNYYIVGNKPPKECGD 180

LCPGTMEEKPMCEKTTINNEYNYRCWTTNRCQKMCPCSTCGKRACTENNECCHPECLGSCS 240

↑ Cyst rich domain →

APDNDTACVACRHYYYAGVCVPACPPNTYRFEGWRCVDRDFCANILSAESSDSEGFVIHD 300

GECMQECPSGFIRNGSQSMYCIPCEGPCPKVCEEKKTKTIDSVTSAQMLQGCTIFKGNL 360

← Cyst rich domain ↑ L2 domain →

LINIRRGNNIASELENFMGLIEVVTGYVKIRHSHALVSLSPFLKNLRLILGEEQLEGNYSP 420

YVLDNQNLQQLWDWDHRNLTIKAGKMYFAPNPKLCVSEIYRMEEVTGKGRQSKGDINTR 480

NNGERASCESDVHLHTTSKNRIITWHRYRPPDYRDLISFTVYYKEAPFKNVTEYDG 540

← L2 ↑ ↑ FbnIII-1 →

QDACGSNSWNMVDVLPPNKDVEPGILLHGLKPWTQYAVYVKAVTLMVENDHIRGAKSE 600

ILYIRTNASVPSIPLDVL SASNSSSQLIVKWNPPSLPNGNL SYYIVRWQRQPQDGYLYRH 660

← FbnIII-1 ↑ FbnIII-2a →

NYCSKDKIPIRKYADGTIDIEEVTEPKTEVGGEKGPCACPKTEAKQAKKEAEYRK 720

VFENPLHNSIFVPRPERKRRDVMQVANTTMSSRSRNNTAADTYNITDPEELETYPFFES 780

Juxtamembranaire α

← Chaîne α / Chaîne β →

RVDNKERTVISNLRPFTLYRIDIHSCNHEAKLGCSASNPFVARTMPAEGADDIPGPVTW 840

↑ FbnIII-2b domain → ← FbnIII-2b ↑ FbnIII-3 →

EPRPENSIFLKWPENPNGLILMYEIKYGSQVEDQRECVSRQBYRKYGGAKLNRLNPGN 900

YTARIQATSLSGNGSWTDPVFFYVQAKTGYENFIHLIIALPVAVLLIVGGLVIMLYVFHR 960

Juxtamembranous β

KRNNNSRLGNGVLYASVNPEYPSAADVYVPDEWEVAREKITMSRELQGSFGMVYEGVAKG 1020

VVKDEPETRAIKTVNEAASMRERIEFLNEASVMKFPNCHVVRLGVVSQGQPTLVIME 1080

**LMTRGDLKSYLRSLRPEMENNPLAPPSSLSKMIQMAQEIAADGMAYLNANKFVRDLAARN 1140**

**CMVAEDPTVKIGDPGMTRDIYETDYRKGGKGLLPVRWMSPESLKDGVFVTTYSDVWSFGV 1200**

**VLWEIATLAEQPYQGLSNEQVLRFVMEGGLLDKPDNCPDMLFELMRMCWQYNPKMRPSFL 1260**

**EIISSIKEEMEPGPREVSFYYSEENKLPEPEELDLEPENMESVPLDPSASSSSLPLPDRH 1320**

**SGHKAENGPGPGLVLRASFDERQPYAHMNGGRKNERALPLPQSSTC 1367**



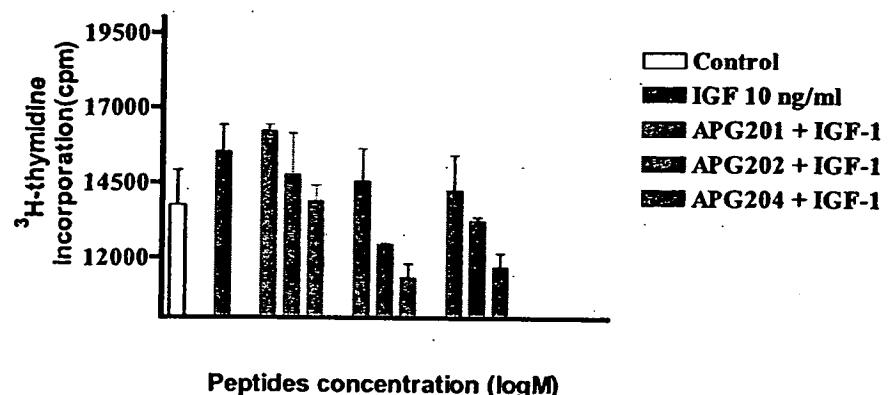
**$\beta$  Chain**

**FIG. 6**

MGWLCSGLLFPVSCLVLLQVASSGNMKVLQEPTCVSDYMSISTCEWKMNNGPTNCSTELRL 60  
 ↑ D1 domain (FbnIII-like) →  
 LYQLVFLSEAHTCIPENNGAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSPKPSEH 120  
 ← D1 ← ↑  
 VKPRAPGNLTVHTNVSDTLLLTWSNPYPDNLYNHLTYAVNISENDPADFRIYNVTYL 180  
 ↑ D2 domain →  
 EPSLRRIAATLKGSIYRARVRAWAQCYNTTWSEWSPSTRWHNSYREPFEQHLLLGVSVS 240  
 ← D2 ↑ Juxtamembranous  
 CIVILAVCLLCYVSITKIKREWWWDQIPNPARSRLVALLIQDAQGSQWEKRSRGQEPAKCP 300  
  
 HWKNCLTKLLPCFLEHNMKRDEDPHKAAKEMPFGSGKSAWCPVEISKTVLWPESISVVR 360  
  
 CVELFEPAPVCEEEEEVEEEEGSFCASPESSRDDFQEGREGIVARLTKESLFLDLLGEENG 420  
  
 GFCQQDMGESCLLPPSGSTS A HMPWDFPSAGPKAAPPWGKEQPLHLEPSP PASPTQSPD 480  
  
 NLTCTETPLVIAGNPAYRSFSNSLSQSPCPRELGPDPILLARHLKEVEP KEMPCVPQLSEPT 540  
  
 TVPQPEPETWEQILRRNVLQHGAAAAPVSAPTSGYQEFVHAVEQGGTQASAVVGLGPPGE 600  
  
 AGYKAFSSLASSAVSPEKCGPGASSGEEGYKPFQDLIPIGCPGDPAPVPVPLFTFGLDR 660  
  
 PPRSPQSSHLPSSSPKHLGLEPGEKVEDMPKPLPQEATDPLVDSLGSIGIVYSALTCHL 720  
  
 CGHLKQCHGQKDGGQTPVMASPCCGCCGDRSSPPTPLRAPDPSPGGVPLEASLCPASL 780  
  
 APSGISEKS KSSSFHPAPGNAQSSSQTPKIVNFVGPTYMRVS 825

FIG. 7

A



B

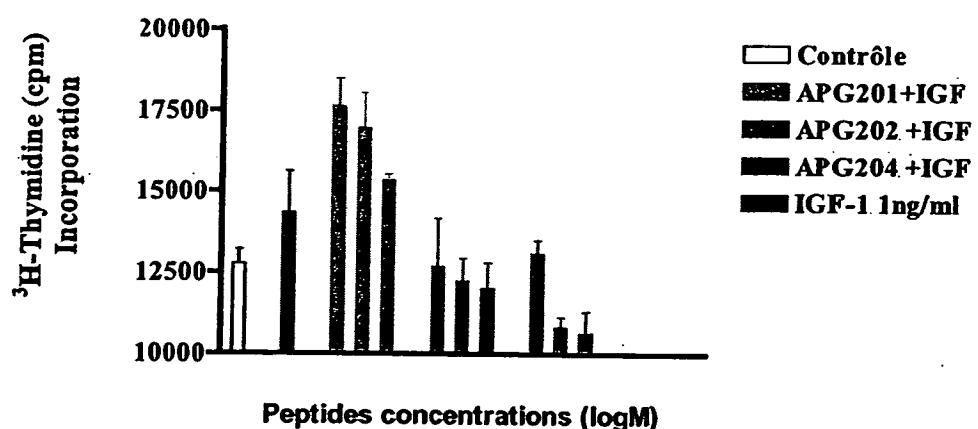
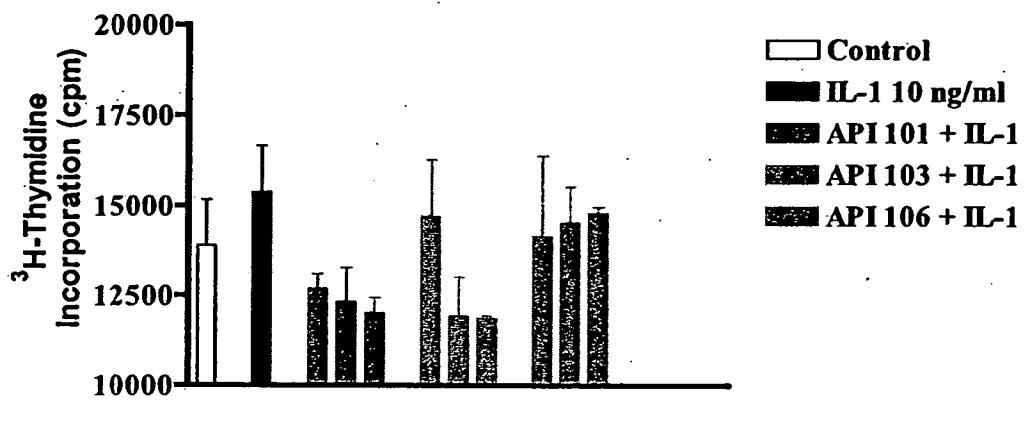


FIG. 8



B

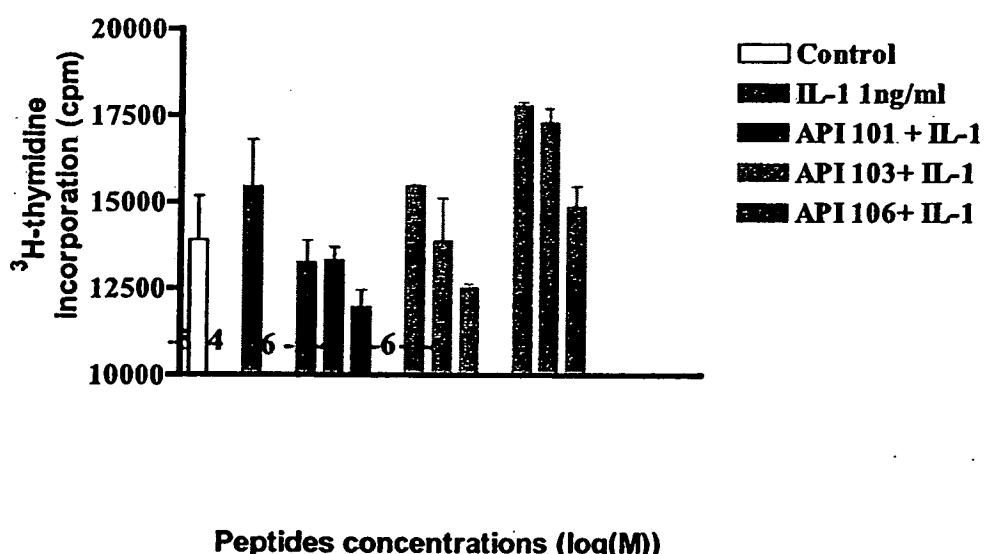


FIG. 9

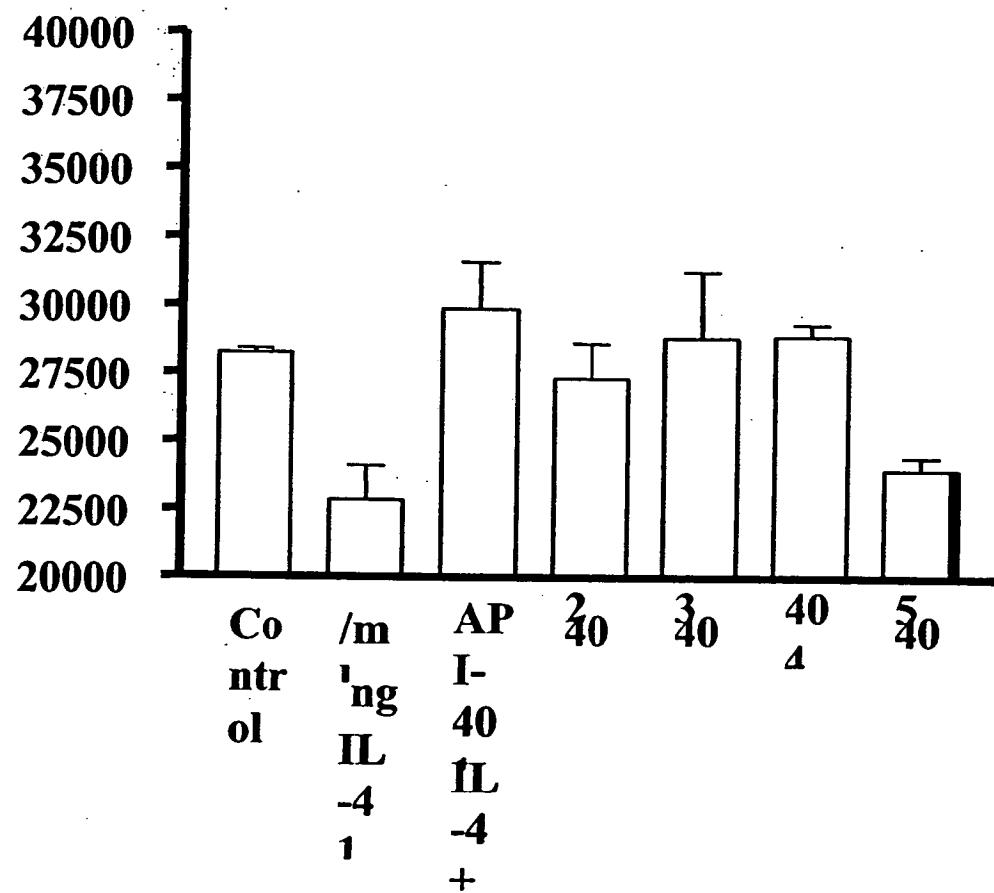


FIG. 10

FIGURE 11

Figure 12

**Figure 13**

VGR2_HUMAN	QLTVLERVAPITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKD
VGR2_MOUSE	QLIILERMAPMITGNLENQTTTIGETIEVTCASGNPTPHITWFKDNETLVEDSGIVLRD
VGR2_RAT	QLVILERMAPMITGNLENQTTTIGETIEVVCPTSGNPTPLITWFKDNETLVEDSGIVLKD
VGR2_QUAIL	HLTVQEPLHPRLVGNLENQTTNIGETIEVLCTNGVPPPNTWFKNSETLFEDSGIVLKD ;*: * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *
VGR2_HUMAN	GNRNLTIIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLEIIILVGTAVIAMF
VGR2_MOUSE	GNRNLTIIRRVRKEDEGGGLYTCQACNVLCARAETLFIIEGAQEKTNLEIIILVGTAVIAMF
VGR2_RAT	GNRNLTIIRRVRKEDEGGGLYTCQACNVLCARAETLFIIEGVQEKTNLEIIILVGTAVIAMF
VGR2_QUAIL	GNKTLTIIRRVRKEDEGGGLYTCACNILGCKKAEAFFSVQGAEEKTNLEIIILVGTAVIAMF ** : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *
VGR2_HUMAN	FWLLLVIILRTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPDRRLKG
VGR2_MOUSE	FWLLLVIILVRTVKRANEGERLKTGYLSIVMDPDELPLDERCERLPYDASKWEFPDRRLKG
VGR2_RAT	FWLLLVIILVRTVKRANEGERLKTGYLSIVMDPDELPLDERCERLPYDASKWEFPDRRLKG
VGR2_QUAIL	FWLLLVIILRTVKRANGGDMKTGYLSIIMDPDEVPIDEHCERLPYDASKWEFPDRRLKG ***** : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *
VGR2_HUMAN	KPLGRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHHLN
VGR2_MOUSE	KPLGRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHHLN
VGR2_RAT	KPLGRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHHLN
VGR2_QUAIL	KPLGRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHHLN ***** : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *
VGR2_HUMAN	VVNLLGACTKPGGPLMVIVEFKFGNLSTYLRSKRNEFPYKTKGARFRQKD-YVGAIP
VGR2_MOUSE	VVNLLGACTKPGGPLMVIVEFSKFGNLSTYLRGKRNEFPYKSKGARFRQKD-YVGELS
VGR2_RAT	VVNLLGACTKPGGPLMVIVEFKFGNLSTYLRGKRNEFPYKSKGARFRSGKD-YVGELS
VGR2_QUAIL	VVNLLGACTKPGGPLMVIVEYCKFGNLSAYLRSKRSEFIPYKMSARFRQKENYTGDIS ***** : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *
VGR2_HUMAN	VDLKRLRDLSDITSSQSSASSGFVVEKSLSDVEEEEAP-EDLYKDFLTLEHLICYSFQVAKG
VGR2_MOUSE	VDLKRLRDLSDITSSQSSASSGFVVEKSLSDVEEEEAS-EELYKDFLTLEHLICYSFQVAKG
VGR2_RAT	VDLKRLRDLSDITSSQSSASSGFVVEKSLSDVEEEEAS-EELYKDFLTLEHLICYSFQVAKG
VGR2_QUAIL	TDLKQRDLSDITSSQSTSSGFVEERSLSDVEEEDAGSEDLCKNPLTMEDLICYSFQVARG .***** : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *
VGR2_HUMAN	MEFLASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKG达尔PKWMAPE
VGR2_MOUSE	MEFLASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKG达尔PKWMAPE
VGR2_RAT	MEFLASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKG达尔PKWMAPE
VGR2_QUAIL	MEFLASRKCIHRDLAARNILLSDNNVVKICDFGLARDIYKDPDYVRKG达尔PKWMAPE ***** : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *
VGR2_HUMAN	TIFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEFCRRLKEGTRMRAPDYTEPEM
VGR2_MOUSE	TIFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEFCRRLKEGTRMRAPDYTEPEM
VGR2_RAT	TIFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEFCRRLKEGTRMRAPDYTEPEM
VGR2_QUAIL	TIFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEFCRRLKEGTRMRAPDYTEPEM ***** : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *
VGR2_HUMAN	YQTMLDCWHGEPSQRPTFSELVEHGNLLQANAQQDGKDYIVLPISETLSMEEDGSLSLP
VGR2_MOUSE	YQTMLDCWHEDPNQRPSFSELVEHGNLLQANAQQDGKDYIVLPMSETLSMEEDGSLSLP
VGR2_RAT	YQTMLDCWHEDPNQRPAFSELVEHGNLLQANAQQDGKDYIVLPMSETLSMEEDGSLSLP
VGR2_QUAIL	YQTMLDCWHGDPKQRPTFSELVEHGNLLQANVRQDGKDYVVLPLSVSINMEEDGSLSLP ***** : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *
VGR2_HUMAN	TSPVSCMEEEEVCDPKHYDNTAGISQYLQNSKRKSRRPVSVKTFEDIPLLEEPEVKVIPDD
VGR2_MOUSE	TSPVSCMEEEEVCDPKHYDNTAGISHYLQNSKRKSRRPVSVKTFEDIPLLEEPEVKVIPDD
VGR2_RAT	TSPVSCMEEEEVCDPKHYDNTAGISHYLQNSKRKSRRPVSVKTFEDIPLLEEPEVKVIPDD
VGR2_QUAIL	TSPASCKEEEVCDPKHYDNTAGISQYRQGSKRKSRRPVSVKTFEDIPLVTT-VKVVQEE *** : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *
VGR2_HUMAN	NQTDGMVLAASEELKTLEDRTK-LSPSFGGMVPSKSRESVAEGSNQTSGYQSGYHSDDT
VGR2_MOUSE	SQTDGMVLAASEELKTLEDRTK-LSPSFGGMVPSKSRESVAEGSNQTSGYQSGYHSDDT
VGR2_RAT	SQTDGMVLAASEELKTLEDRTK-LSPSFGGMVPSKSRESVAEGSNQTSGYQSGYHSDDT
VGR2_QUAIL	NQTDGMVLAASEELKTLEEQDKQVKIPFSTLAPSNSNESVMSEASNQTSGYQSGYHSDDM .***** : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

Figure 13 (continued)

VGR2\_HUMAN DTTVYSSEEAEELLKLIIEIGVQTGSTAQILQPDSGTTLSSPPV-----  
VGR2\_MOUSE DTTVYSSEAGLLKMVDAAVHADSGTTLQLTSCLNNSGPVPAPPPTPGNHERGAA  
VGR2\_RAT DTTVYSSEAGLLKLVDVAGHVDSGTTLRSSPV-----  
VGR2\_QUAIL DNMVCSSEDTELLCAQEASPTLPRCAWPGIYSPAPVASLPL-----  
\* \* \* \*; : \* :

Figure 13 (continued)